A. Navarro

1645

P#9

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       RAW SEQUENCE LISTING                    DATE: 07/30/2002
       PATENT APPLICATION:  US/09/684,883      TIME: 14:21:00

       Input Set : N:\Crf3\RULE60\09684883.raw
       Output Set: N:\CRF3\07302002\I684883.raw

       SEQUENCE LISTING
 3  (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Brodeur, Bernard R
 6                     Martin, Denis
 7                     Hamel, Josee
 8                     Rioux, Clement
10     (ii) TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
11                              OF NEISSERIA MENINGITIDIS
13    (iii) NUMBER OF SEQUENCES: 30
15     (iv) CORRESPONDENCE ADDRESS:
16          (A) ADDRESSEE: Foley & Lardner
17          (B) STREET: 3000 K Street, N.W., Suite 500
18          (C) CITY: Washington
19          (D) STATE: D.C.
20          (E) COUNTRY: USA
21          (F) ZIP: 20007-5109
23      (v) COMPUTER READABLE FORM:
24          (A) MEDIUM TYPE: Floppy disk
25          (B) COMPUTER: IBM PC compatible
26          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29     (vi) CURRENT APPLICATION DATA:
30          (A) APPLICATION NUMBER: US/09/684,883
31          (B) FILING DATE: 06-Oct-2000
42    (vii) PRIOR APPLICATION DATA:
34          (A) APPLICATION NUMBER: US/08/913,362
35          (B) FILING DATE: 13-NOV-1997
39          (A) APPLICATION NUMBER: US 08/406,362
40          (B) FILING DATE: 17-MAR-1995
43          (A) APPLICATION NUMBER: US 60/001,983
44          (B) FILING DATE: 04-AUG-1995
46   (viii) ATTORNEY/AGENT INFORMATION:
47          (A) NAME: Bent, Stephen A.
48          (B) REGISTRATION NUMBER: 29,768
49          (C) REFERENCE/DOCKET NUMBER: 047998/0128
51     (ix) TELECOMMUNICATION INFORMATION:
52          (A) TELEPHONE: (202)672-5300
53          (B) TELEFAX: (202)672-5399
54          (C) TELEX: 904136
57  (2) INFORMATION FOR SEQ ID NO: 1:
59      (i) SEQUENCE CHARACTERISTICS:
60          (A) LENGTH: 830 base pairs
61          (B) TYPE: nucleic acid
```

C--> 30
C--> 31

RAW SEQUENCE LISTING   DATE: 07/30/2002
PATENT APPLICATION: US/09/684,883   TIME: 14:21:00

        Input Set : N:\Crf3\RULE60\09684883.raw
        Output Set: N:\CRF3\07302002\I684883.raw

```
62           (C) STRANDEDNESS: double
63           (D) TOPOLOGY: linear
65     (ii) MOLECULE TYPE: DNA (genomic)
67    (iii) HYPOTHETICAL: NO
69     (iv) ANTI-SENSE: NO
71     (vi) ORIGINAL SOURCE:
72           (A) ORGANISM: Neisseria meningitidis
73           (B) STRAIN: 608B
75     (ix) FEATURE:
76           (A) NAME/KEY: CDS
77           (B) LOCATION: 143..667
79     (ix) FEATURE:
80           (A) NAME/KEY: sig_peptide
81           (B) LOCATION: 143..199
83     (ix) FEATURE:
84           (A) NAME/KEY: mat_peptide
85           (B) LOCATION: 200..667
88     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
90 TCGGCAAAGC AGCCGGATAC CGCTACGTAT CTTGAAGTAT TGAAAATATT ACGATGCAAA  60
92 AAAGAAAATT TAAGTATAAT ACAGCAGGAT TCTTTAACGG ATTCTTAACA ATTTTTCTAA 120
94 CTGACCATAA AGGAACCAAA AT ATG AAA AAA GCA CTT GCC ACA CTG ATT GCC 172
95                        Met Lys Lys Ala Leu Ala Thr Leu Ile Ala
96                        -19            -15               -10
98 CTC GCT CTC CCG GCC GCC GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC  220
99 Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr
100               -5                  1               5
102 GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA GGT TCT  268
103 Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu Gly Ser
104           10                  15                  20
106 GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC  316
107 Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp
108       25                  30                  35
110 CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA  364
111 Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro
112   40                  45                  50                  55
114 TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC  412
115 Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp
116               60                  65                  70
118 TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC  460
119 Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser
120               75                  80                  85
122 CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC AGC CAA  508
123 Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln
124           90                  95                  100
126 ACC TCC ATC GGC CTC GGC GTA TTG ACG GGC GTA AGC TAT GCC GTT ACC  556
127 Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr Ala Val Thr
128       105                 110                 115
130 CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA  604
131 Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys
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RAW SEQUENCE LISTING   DATE: 07/30/2002
PATENT APPLICATION: US/09/684,883   TIME: 14:21:00

            Input Set : N:\Crf3\RULE60\09684883.raw
            Output Set: N:\CRF3\07302002\I684883.raw

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132 120                 125             130             135
134 GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GTC GGC GTG   652
135 Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Val Gly Val
136                 140             145             150
138 CGC GTC AAA TTC TGATATGCGC CTTATTCTGC AAACCGCCGA GCCTTCGGCG   704
139 Arg Val Lys Phe
140                 155
142 GTTTTGTTTT CTGCCACCGC AACTACACAA GCCGGCGGTT TTGTACGATA ATCCCGAATG 764
144 CTGCGGCTTC TGCCGCCCTA TTTTTTGAGG AATCCGAAAT GTCCAAAACC ATCATCCACA 824
146 CCGACA                                                     830
149 (2) INFORMATION FOR SEQ ID NO: 2:
151      (i) SEQUENCE CHARACTERISTICS:
152           (A) LENGTH: 174 amino acids
153           (B) TYPE: amino acid
154           (D) TOPOLOGY: linear
156      (ii) MOLECULE TYPE: protein
158      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
160 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala
161 -19             -15             -10             -5
163 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
164             1               5               10
166 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
167      15              20              25
169 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
170 30              35              40              45
172 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu
173             50              55              60
175 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
176             65              70              75
178 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
179      80              85              90
181 Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile Gly Leu Gly
182      95              100             105
184 Val Leu Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
185 110             115             120             125
187 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
188             130             135             140
190 Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe
191             145             150             155
194 (2) INFORMATION FOR SEQ ID NO: 3:
196      (i) SEQUENCE CHARACTERISTICS:
197           (A) LENGTH: 710 base pairs
198           (B) TYPE: nucleic acid
199           (C) STRANDEDNESS: double
200           (D) TOPOLOGY: linear
202      (ii) MOLECULE TYPE: DNA (genomic)
204      (iii) HYPOTHETICAL: NO
206      (iv) ANTI-SENSE: NO
208      (vi) ORIGINAL SOURCE:
```

RAW SEQUENCE LISTING   DATE: 07/30/2002
PATENT APPLICATION: US/09/684,883   TIME: 14:21:00

Input Set : N:\Crf3\RULE60\09684883.raw
Output Set: N:\CRF3\07302002\I684883.raw

```
209           (A) ORGANISM: Neisseria meningitidis
210           (B) STRAIN: MCH88
212     (ix) FEATURE:
213           (A) NAME/KEY: CDS
214           (B) LOCATION: 116..643
216     (ix) FEATURE:
217           (A) NAME/KEY: sig_peptide
218           (B) LOCATION: 116..172
220     (ix) FEATURE:
221           (A) NAME/KEY: mat_peptide
222           (B) LOCATION: 173..643
225     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
227 GTATCTTGAG GCATTGAAAA TATTACAATG CAAAAAGAAA ATTTCAGTAT AATACGGCAG  60
229 GATTCTTTAA CGGATTCTTA ACCATTTTTC TCCCTGACCA TAAAGGAATC AAGAT ATG  118
230                                                              Met
231                                                              -19
233 AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCC CTC CCG GCC GCC GCA  166
234 Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala Ala
235             -15                 -10                 -5
237 CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA CAC  214
238 Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His
239           1                 5                 10
241 GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG CGC  262
242 Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro Arg
243 15                  20                  25                  30
245 ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT TAC  310
246 Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr
247             35                  40                  45
249 ACG CGC TAC AAA AAC TAT AAA CAA GTC CCA TCC ACC GAT TTC AAA CTT  358
250 Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys Leu
251             50                  55                  60
253 TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC TTC GAC ACC CAA TCC CCC  406
254 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
255             65                  70                  75
257 GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC CTC AAC CGC GCC TCC GTC  454
258 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
259 80                  85                  90
261 GAC TTT AAC GGC AGC GAC AGC TTC AGC CAA ACC TCC ACC GGC CTC GGC  502
262 Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly
263 95                  100                 105                 110
265 GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT  550
266 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
267             115                 120                 125
269 GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA GTC AAC ACT GTC AAA AAT  598
270 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
271             130                 135                 140
273 GTC CGT TCC GGC GAA CTG TCC GCC GGC GTA CGC GTC AAA TTC TGATATACGC 650
274 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
275             145                 150                 155
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RAW SEQUENCE LISTING   DATE: 07/30/2002
PATENT APPLICATION: US/09/684,883   TIME: 14:21:00

Input Set : **N:\Crf3\RULE60\09684883.raw**
Output Set: **N:\CRF3\07302002\I684883.raw**

```
277 GTTATTCCGC AAACCGCCGA GCCTTTCGGC GGTTTTGTTT TCCGCCGCCG CAACTACACA   710
281 (2) INFORMATION FOR SEQ ID NO: 4:
283     (i) SEQUENCE CHARACTERISTICS:
284         (A) LENGTH: 175 amino acids
285         (B) TYPE: amino acid
286         (D) TOPOLOGY: linear
288     (ii) MOLECULE TYPE: protein
290     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
292 Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala
293 -19             -15             -10              -5
295 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
296             1               5               10
298 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
299     15              20              25
301 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
302 30              35              40              45
304 Tyr Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys
305             50              55              60
307 Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser
308             65              70              75
310 Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser
311         80              85              90
313 Val Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu
314     95              100             105
316 Gly Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu
317 110             115             120             125
319 Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys
320             130             135             140
322 Asn Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
323             145             150             155
326 (2) INFORMATION FOR SEQ ID NO: 5:
328     (i) SEQUENCE CHARACTERISTICS:
329         (A) LENGTH: 850 base pairs
330         (B) TYPE: nucleic acid
331         (C) STRANDEDNESS: double
332         (D) TOPOLOGY: linear
334     (ii) MOLECULE TYPE: DNA (genomic)
336    (iii) HYPOTHETICAL: NO
338     (iv) ANTI-SENSE: NO
340     (vi) ORIGINAL SOURCE:
341         (A) ORGANISM: Neisseria meningitidis
342         (B) STRAIN: Z4063
344     (ix) FEATURE:
345         (A) NAME/KEY: CDS
346         (B) LOCATION: 208..732
348     (ix) FEATURE:
349         (A) NAME/KEY: sig_peptide
350         (B) LOCATION: 208..264
352     (ix) FEATURE:
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/30/2002
PATENT APPLICATION: US/09/684,883   TIME: 14:21:01

Input Set : **N:\Crf3\RULE60\09684883.raw**
Output Set: **N:\CRF3\07302002\I684883.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:30; Xaa Pos.7,73,126

VERIFICATION SUMMARY   DATE: 07/30/2002
PATENT APPLICATION: **US/09/684,883**   TIME: 14:21:01

Input Set : **N:\Crf3\RULE60\09684883.raw**
Output Set: **N:\CRF3\07302002\I684883.raw**

```
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:64
L:1071 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:112
```